

SEQUENCE LISTING

<110> KAPELLER-LIBERMANN
SILOS-SANTIAGO

<120> METHODS OF USING 18903 TO TREAT PAIN AND
PAIN-RELATED DISORDERS

<130> MNI-199

<150> 60/250929

<151> 2000-11-30

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1983

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)...(1849)

<400> 1

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cca tcc aca gtg ttg cca tca ctc ctg ccc aca gca gga gct ggc tgg 163
Pro Ser Thr Val Leu Pro Ser Leu Leu Pro Thr Ala Gly Ala Gly Trp
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Ser Met Arg Trp Ile Leu Cys Trp Ser Leu Thr Leu Cys Leu Met Ala
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cag acg gcc ttg ggt gcc ttg cac acc aag agg cct caa gtg gtc acc 259
Gln Thr Ala Leu Gly Ala Leu His Thr Lys Arg Pro Gln Val Val Thr
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Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met His Val Gly Lys Thr Pro
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Ile Gln Val Phe Leu Gly Val Pro Phe Ser Arg Pro Pro Leu Gly Ile
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ctc agg ttt gca cct cca gaa ccc ccg gag ccc tgg aaa gga atc aga 403
Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu Pro Trp Lys Gly Ile Arg
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gat gct acc acc tac ccg cct ggg tgc ctg cag gag tcc tgg ggc cag 451
Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu Gln Glu Ser Trp Gly Gln
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 <212> PRT
 <213> Homo sapiens

<400> 2

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Ile	Ile	Trp	Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp
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 Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly
 450 455 460
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 465 470 475 480
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 Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys
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<220>
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 <222> (1)...(1752)

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 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
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 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
 65 70 75 80
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 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
 85 90 95
 ccc tgg aaa gga atc aga gat gct acc acc tac ccg cct ggg tgc ctg 336
 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
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 cag gag tcc tgg ggc cag ctg gcc tcg atg tac gtc agc acg cgg gaa 384

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tac	gcg	ccg	gcg	cgc	gcg	ccc	ggg	gat	ccc	cag	ctg	cca	gtg	atg	gtc	480
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	Val	
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<223> Xaa may be any amino acid

<221> VARIANT

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<223> Xaa may be Leu, Ile, Met or Val

<221> VARIANT

<222> 10

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 15

<223> Xaa may be Ser, Thr, Ala, or Gly

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<210> 5

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Xaa may be Tyr or Thr

<221> VARIANT

<222> 6,8

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 7

<223> Asp, Asn, or Ser

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<223> Xaa may be Leu, Ile, Phe, Tyr, Trp or Val

<221> VARIANT

<222> (10)...(10)

<223> Xaa may be any amino acid

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<222> (11)...(11)

<223> Xaa may be Pro, Gln or Arg

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<210> 6

<211> 2456

<212> DNA

<213> Homo sapiens

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 <212> PRT
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Met	Ser	Thr	Gly	Phe	Ser	Phe	Gly	Ser	Gly	Thr	Leu	Gly	Ser	Thr	Thr
1				5					10					15	
Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe	Gly	Thr
			20					25					30		
Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly	Asn	Leu	Gly
		35					40					45			
Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser	Ser	Gly	Phe	Gly
	50					55					60				
Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly	Phe	Thr	Leu	Gly	Gly
65					70					75					80
Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg	Pro	Gln	Val	Val	Thr	Lys
				85					90					95	
Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met	His	Val	Gly	Lys	Thr	Pro	Ile
			100					105					110		
Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu
			115					120					125		
Arg	Phe	Ala	Pro	Pro	Glu	Pro	Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp
			130				135					140			
Ala	Thr	Thr	Tyr	Pro	Pro	Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp
145					150					155					160
Ser	Ala	Val	Ala	Arg	Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val
				165					170					175	
Gln	Ala	Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys
			180					185					190		
Leu	Gln	Glu	Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg
			195				200					205			
Glu	Arg	Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn
		210				215					220				
Val	Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met
225					230					235					240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	Tyr
				245					250					255	
Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	Phe	Leu
			260					265					270		
Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	Asp	Ser	His
			275					280					285		
Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	Ala	Leu	Arg	Trp
			290			295					300				
Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Asn	Val	Thr
305					310					315					320
Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	Ile	Ser	Gly	Leu	Met	Met
				325					330					335	
Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	Arg	Ala	Ile	Ser	Gln	Ser	Gly
			340					345					350		
Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala
			355				360						365		
Lys	Lys	Val	Ala	His	Leu	Ala	Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile
			370			375					380				
Leu	Val	Asn	Cys	Leu	Arg	Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val
385					390					395					400
Ser	Asn	Lys	Met	Arg	Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu
				405					410				415		
Glu	Ile	Ile	Trp	Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro

420 425 430
Asp Asp Pro Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro
435 440 445
Tyr Leu Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr
450 455 460
Asn Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp
465 470 475 480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met Asp
485 490 495
Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr Ala His
500 505 510
Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala Gly His Ala
515 520 525
Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu Pro Gln Glu Trp
530 535 540
Ala
545